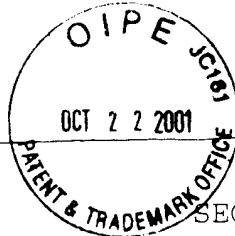


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OCT 22 2001

TECH CENTER 1600, 2900



SEQUENCE LISTING

<110> ARNOLD, Frances H.
PETROUNIA, Ionna P.
SUN, Lianhong

<120> DIRECTED EVOLUTION OF OXIDASE ENZYMES

<130> 9373/1G811US1

<140> 09/722,602

<141> 2000-11-27

<150> US 09/571,553

<151> 2000-05-16

<160> 48

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 1

aattcgaagc ttatggcctc agcacctatc ggaagc

36

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<211> 33

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<213> Artificial Sequence

<220>

<223> Primer

<400> 2

cttccttcta gattactgag taacgcgaat cgt

33

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 3

ggaagagaat tcaatacgca aaccgcctct 30
<210> 4
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
ggtcataaggc ttttcctgtg tgaaattgtt at 32
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<223> Primer

<400> 5
accatgattt cgacgtcggt accctcagca 30
<210> 6
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<220>
<223> Primer

<400> 6
cttcctaaggc tttcactgag taacgcgaat 30
<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

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<223> Primer

<400> 7
ggaagaggta ccaatacgca aaccgcctct 30
<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8

ttgttcctgc ggctgcagca attgaaccg

29

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 9

tgcgggtcga ctctagatta ctgagtaacg

30

<210> 10

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 9.16.8D2 (N537D) of D. dendroides GaO

<400> 10

Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
1 5 10 15
Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
20 25 30
Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
35 40 45
Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
50 55 60
Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
65 70 75 80
Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
85 90 95
Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
100 105 110
Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
115 120 125
Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
130 135 140
Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
145 150 155 160
Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ile
165 170 175
Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
180 185 190
Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
195 200 205
Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
210 215 220
Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val

225	230	235	240
Val Thr Gly Gly Asn Asp Ala Lys Lys	Thr Ser Leu Tyr Asp Ser Ser		
245	250	255	
Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg	Gly Tyr		
260	265	270	
Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr	Ile Gly Gly		
275	280	285	
Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val	Tyr Ser Pro		
290	295	300	
Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met			
305	310	315	320
Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp			
325	330	335	
Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr			
340	345	350	
Ala Met Asn Trp Tyr Tyr Ser Gly Ser Gly Asp Val Lys Ser Ala			
355	360	365	
Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly			
370	375	380	
Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly			
385	390	395	400
Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile			
405	410	415	
Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser			
420	425	430	
Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro			
435	440	445	
Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe			
450	455	460	
Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln			
465	470	475	480
Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Val Tyr His			
485	490	495	
Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly			
500	505	510	
Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe			
515	520	525	
Thr Pro Asn Tyr Leu Tyr Asn Ser Asp Gly Asn Leu Ala Thr Arg Pro			
530	535	540	
Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile			
545	550	555	560
Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr			
565	570	575	
Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu			
580	585	590	
Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser			
595	600	605	
Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn			
610	615	620	
Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln			
625	630	635	

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 9.16.6C11 (V494A, C515S) of D. dendroides
GaO

<400> 11

Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
1 5 10 15
Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
20 25 30
Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
35 40 45
Pro Lys Pro Pro His Thr Tyr Ile Asp Met Lys Thr Thr Gln Asn
50 55 60
Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
65 70 75 80
Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
85 90 95
Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
100 105 110
Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
115 120 125
Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
130 135 140
Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
145 150 155 160
Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ile
165 170 175
Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
180 185 190
Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
195 200 205
Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
210 215 220
Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
225 230 235 240
Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
245 250 255
Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
260 265 270
Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
275 280 285
Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
290 295 300
Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
305 310 315 320
Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
325 330 335
Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
340 345 350

Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
 355 360 365
 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
 370 375 380
 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
 385 390 395 400
 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
 405 410 415
 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
 420 425 430
 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
 435 440 445
 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
 450 455 460
 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
 465 470 475 480
 Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala Tyr His
 485 490 495
 Ser Ile Ser Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
 500 505 510
 Gly Leu Ser Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
 515 520 525
 Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro
 530 535 540
 Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
 545 550 555 560
 Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
 565 570 575
 Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
 580 585 590
 Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
 595 600 605
 Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
 610 615 620
 Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
 625 630 635

<210> 12
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 9.16.16D12 (P136, V494A) of D. dendroides
 GaO

<400> 12
 Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
 1 5 10 15
 Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
 20 25 30
 Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
 35 40 45

Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
 50 55 60
 Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
 65 70 75 80
 Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
 85 90 95
 Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
 100 105 110
 Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
 115 120 125
 Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
 130 135 140
 Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
 145 150 155 160
 Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile
 165 170 175
 Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
 180 185 190
 Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
 195 200 205
 Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
 210 215 220
 Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
 225 230 235 240
 Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
 245 250 255
 Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
 260 265 270
 Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
 275 280 285
 Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
 290 295 300
 Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
 305 310 315 320
 Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
 325 330 335
 Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
 340 345 350
 Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
 355 360 365
 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
 370 375 380
 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
 385 390 395 400
 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
 405 410 415
 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
 420 425 430
 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
 435 440 445
 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
 450 455 460
 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln

465	470	475	480
Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala Tyr His			
485	490	495	
Ser Ile Ser Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly			
500	505	510	
Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe			
515	520	525	
Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro			
530	535	540	
Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile			
545	550	555	560
Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr			
565	570	575	
Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu			
580	585	590	
Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser			
595	600	605	
Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn			
610	615	620	
Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln			
625	630	635	

<210> 13

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 11.03.6D3 (S10P, P136, V494A) of D.
dendroides GaO

<400> 13

Ala Ser Ala Pro Ile Gly Ser Ala Ile Pro Arg Asn Asn Trp Ala Val			
1	5	10	15
Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp			
20	25	30	
Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp			
35	40	45	
Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn			
50	55	60	
Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly			
65	70	75	80
Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp			
85	90	95	
Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys			
100	105	110	
Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala			
115	120	125	
Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn			
130	135	140	
Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg			
145	150	155	160
Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ile			

	165	170	175												
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
	180					185							190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
	195					200							205		
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215							220		
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
	225					230							235		240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
							245						250		255
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
							260						265		270
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
							275						280		285
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
							290						295		300
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
							305						310		320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
							325						330		335
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
							340						345		350
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
							355						360		365
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
							370						375		380
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
							385						390		400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile
							405						410		415
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
							420						425		430
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
							435						440		445
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
							450						455		460
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
							465						470		480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
							485						490		495
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
							500						505		510
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
							515						520		525
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
							530						535		540
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
							545						550		560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
							565						570		575
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
							580						585		590

Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
595 600 605
Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
610 615 620
Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
625 630 635

<210> 14

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 11.03.10C3 (A3, P136, G195E, V494A) of D.
dendroides GaO

<400> 14

Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
1 5 10 15
Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
20 25 30
Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
35 40 45
Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
50 55 60
Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
65 70 75 80
Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
85 90 95
Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
100 105 110
Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
115 120 125
Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
130 135 140
Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
145 150 155 160
Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ile
165 170 175
Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
180 185 190
Ala Phe Glu Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
195 200 205
Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
210 215 220
Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
225 230 235 240
Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
245 250 255
Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
260 265 270
Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
275 280 285

Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
 290 295 300
 Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
 305 310 315 320
 Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
 325 330 335
 Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
 340 345 350
 Ala Met Asn Trp Tyr Tyr Ser Gly Ser Gly Asp Val Lys Ser Ala
 355 360 365
 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
 370 375 380
 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
 385 390 395 400
 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
 405 410 415
 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
 420 425 430
 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
 435 440 445
 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
 450 455 460
 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
 465 470 475 480
 Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala Tyr His
 485 490 495
 Ser Ile Ser Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly
 500 505 510
 Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
 515 520 525
 Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro
 530 535 540
 Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
 545 550 555 560
 Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
 565 570 575
 Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
 580 585 590
 Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
 595 600 605
 Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
 610 615 620
 Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
 625 630 635

<210> 15

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 11.03.10D6 (P136, T218, L312, V494A, N535D)
of D. dendroides GaO

<400> 15

Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
1 5 10 15
Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
20 25 30
Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
35 40 45
Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
50 55 60
Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
65 70 75 80
Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
85 90 95
Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
100 105 110
Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
115 120 125
Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
130 135 140
Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
145 150 155 160
Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ile
165 170 175
Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
180 185 190
Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
195 200 205
Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
210 215 220
Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
225 230 235 240
Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
245 250 255
Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
260 265 270
Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
275 280 285
Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
290 295 300
Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
305 310 315 320
Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
325 330 335
Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
340 345 350
Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
355 360 365
Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
370 375 380
Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
385 390 395 400
Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile

	405		410		415										
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
				420				425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
					435			440					445		
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
					450			455					460		
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
					465			470			475			480	
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
					485				490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
					500				505					510	
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
					515				520					525	
Thr	Pro	Asn	Tyr	Leu	Tyr	Asp	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
					530				535					540	
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
					545				550					560	
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
					565				570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
					580				585					590	
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
					595				600					605	
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
					610				615					620	
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
					625				630					635	

<210> 16

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 11.03.13E12 (M70V, P136, V494A) from D.
Dendroides GaO

<400> 16

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5				10					15		
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
					20				25				30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
					35				40				45		
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
					50				55				60		
Val	Asn	Gly	Leu	Ser	Val	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
					65				70				75		80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
					85				90				95		
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys

100	105	110	
Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg	Leu Val Ala		
115	120	125	
Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn			
130	135	140	
Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg			
145	150	155	160
Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile			
165	170	175	
Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp			
180	185	190	
Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp			
195	200	205	
Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His			
210	215	220	
Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val			
225	230	235	240
Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser			
245	250	255	
Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr			
260	265	270	
Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly			
275	280	285	
Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro			
290	295	300	
Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met			
305	310	315	320
Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp			
325	330	335	
Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr			
340	345	350	
Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala			
355	360	365	
Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly			
370	375	380	
Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly			
385	390	395	400
Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile			
405	410	415	
Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser			
420	425	430	
Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro			
435	440	445	
Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe			
450	455	460	
Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln			
465	470	475	480
Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala Tyr His			
485	490	495	
Ser Ile Ser Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly			
500	505	510	
Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe			
515	520	525	

Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro
 530 535 540
 Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
 545 550 555 560
 Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
 565 570 575
 Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
 580 585 590
 Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
 595 600 605
 Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
 610 615 620
 Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
 625 630 635

<210> 17

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 1.06.20E7 (S10P, M70V, P136, G195E, V494A, N535D) from D. Dendroides GaO

<400> 17

Ala Ser Ala Pro Ile Gly Ser Ala Ile Pro Arg Asn Asn Trp Ala Val
 1 5 10 15
 Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
 20 25 30
 Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
 35 40 45
 Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
 50 55 60
 Val Asn Gly Leu Ser Val Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
 65 70 75 80
 Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
 85 90 95
 Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
 100 105 110
 Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
 115 120 125
 Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
 130 135 140
 Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
 145 150 155 160
 Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ile
 165 170 175
 Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
 180 185 190
 Ala Phe Glu Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
 195 200 205
 Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
 210 215 220

Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
 225 230 235 240
 Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
 245 250 255
 Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
 260 265 270
 Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
 275 280 285
 Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
 290 295 300
 Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
 305 310 315 320
 Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
 325 330 335
 Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
 340 345 350
 Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
 355 360 365
 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
 370 375 380
 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
 385 390 395 400
 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
 405 410 415
 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
 420 425 430
 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
 435 440 445
 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
 450 455 460
 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
 465 470 475 480
 Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala Tyr His
 485 490 495
 Ser Ile Ser Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
 500 505 510
 Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
 515 520 525
 Thr Pro Asn Tyr Leu Tyr Asp Ser Asn Gly Asn Leu Ala Thr Arg Pro
 530 535 540
 Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
 545 550 555 560
 Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
 565 570 575
 Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
 580 585 590
 Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
 595 600 605
 Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
 610 615 620
 Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
 625 630 635

<210> 18

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 1.D4 (N413D) from D. Dendroides GaO

<400> 18

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5				10						15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
					20			25						30	
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
						35		40			45				
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
						50		55			60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
					65		70		75					80	
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
						85		90						95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
					100			105						110	
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
					115			120					125		
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
					130			135				140			
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
					145		150			155				160	
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ile	
						165			170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
						180			185					190	
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
						195		200			205				
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
						210		215			220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
						225		230			235			240	
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
						245			250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
						260		265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
						275		280				285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
						290		295			300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
						305		310			315			320	
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
						325			330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
						340			345					350	

Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
 355 360 365
 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
 370 375 380
 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
 385 390 395 400
 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asp Ala His Ile
 405 410 415
 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
 420 425 430
 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
 435 440 445
 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
 450 455 460
 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
 465 470 475 480
 Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Val Tyr His
 485 490 495
 Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly
 500 505 510
 Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
 515 520 525
 Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro
 530 535 540
 Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
 545 550 555 560
 Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
 565 570 575
 Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
 580 585 590
 Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
 595 600 605
 Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
 610 615 620
 Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
 625 630 635

<210> 19

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 2.G4 (N413D, S550) from D. Dendroides GaO

<400> 19

Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
 1 5 10 15
 Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
 20 25 30
 Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
 35 40 45
 Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn

50	55	60	
Val Asn Gly Leu Ser Met	Leu Pro Arg Gln Asp	Gly Asn Gln Asn Gly	
65	70	75	80
Trp Ile Gly Arg His Glu Val Tyr	Leu Ser Ser Asp Gly	Thr Asn Trp	
85	90	95	
Gly Ser Pro Val Ala Ser Gly	Ser Trp Phe Ala Asp Ser	Thr Thr Lys	
100	105	110	
Tyr Ser Asn Phe Glu Thr Arg	Pro Ala Arg Tyr Val Arg	Leu Val Ala	
115	120	125	
Ile Thr Glu Ala Asn Gly	Gln Pro Trp Thr Ser	Ile Ala Glu Ile Asn	
130	135	140	
Val Phe Gln Ala Ser Ser	Tyr Thr Ala Pro Gln Pro	Gly Leu Gly Arg	
145	150	155	160
Trp Gly Pro Thr Ile Asp	Leu Pro Ile Val Pro	Ala Ala Ala Ala Ile	
165	170	175	
Glu Pro Thr Ser Gly Arg	Val Leu Met Trp Ser	Ser Tyr Arg Asn Asp	
180	185	190	
Ala Phe Gly Gly Ser Pro	Gly Ile Thr Leu Thr	Ser Ser Trp Asp	
195	200	205	
Pro Ser Thr Gly Ile Val	Ser Asp Arg Thr Val	Thr Val Thr Lys His	
210	215	220	
Asp Met Phe Cys Pro Gly	Ile Ser Met Asp Gly	Asn Gly Gln Ile Val	
225	230	235	240
Val Thr Gly Gly Asn Asp	Ala Lys Lys Thr	Ser Leu Tyr Asp Ser Ser	
245	250	255	
Ser Asp Ser Trp Ile Pro	Gly Pro Asp Met Gln	Val Ala Arg Gly Tyr	
260	265	270	
Gln Ser Ser Ala Thr Met	Ser Asp Gly Val Phe	Thr Ile Gly Gly	
275	280	285	
Ser Trp Ser Gly Gly Val	Phe Glu Lys Asn Gly	Glu Val Tyr Ser Pro	
290	295	300	
Ser Ser Lys Thr Trp	Thr Ser Leu Pro Asn	Ala Lys Val Asn Pro Met	
305	310	315	320
Leu Thr Ala Asp Lys	Gln Gly Leu Tyr Arg	Ser Asp Asn His Ala Trp	
325	330	335	
Leu Phe Gly Trp Lys Lys	Gly Ser Val Phe Gln	Ala Gly Pro Ser Thr	
340	345	350	
Ala Met Asn Trp Tyr Tyr	Thr Ser Gly Asp Val	Lys Ser Ala	
355	360	365	
Gly Lys Arg Gln Ser Asn	Arg Gly Val Ala Pro	Asp Ala Met Cys Gly	
370	375	380	
Asn Ala Val Met Tyr	Asp Ala Val Lys Gly	Lys Ile Leu Thr Phe Gly	
385	390	395	400
Gly Ser Pro Asp Tyr	Gln Asp Ser Asp Ala	Thr Thr Asp Ala His Ile	
405	410	415	
Ile Thr Leu Gly Glu	Pro Gly Thr Ser	Pro Asn Thr Val Phe Ala Ser	
420	425	430	
Asn Gly Leu Tyr Phe	Ala Arg Thr Phe His	Thr Ser Val Val Leu Pro	
435	440	445	
Asp Gly Ser Thr Phe Ile	Thr Gly Gly Gln Arg	Arg Gly Ile Pro Phe	
450	455	460	
Glu Asp Ser Thr Pro Val	Phe Thr Pro Glu Ile	Tyr Val Pro Glu Gln	
465	470	475	480

Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Val	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
				500				505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
				515			520				525				
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
				530			535				540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545				550					555					560	
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565				570					575		
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
				580				585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
				595				600				605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
				610			615			620					
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
				625				630			635				

<210> 20

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 3.H7 (N413D, S550, V494A) from D.
Dendroides GaO

<400> 20

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
				20				25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
				35				40			45				
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
				50				55			60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
				65				70			75			80	
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85				90					95		
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
				100				105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
				115				120					125		
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
				130				135			140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
				145				150			155			160	
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ile	
				165					170				175		

Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
 180 185 190
 Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
 195 200 205
 Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
 210 215 220
 Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
 225 230 235 240
 Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser
 245 250 255
 Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
 260 265 270
 Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
 275 280 285
 Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
 290 295 300
 Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
 305 310 315 320
 Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
 325 330 335
 Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
 340 345 350
 Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
 355 360 365
 Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
 370 375 380
 Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
 385 390 395 400
 Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asp Ala His Ile
 405 410 415
 Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser
 420 425 430
 Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
 435 440 445
 Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
 450 455 460
 Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
 465 470 475 480
 Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala Tyr His
 485 490 495
 Ser Ile Ser Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
 500 505 510
 Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
 515 520 525
 Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro
 530 535 540
 Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
 545 550 555 560
 Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
 565 570 575
 Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
 580 585 590
 Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser

595	600	605
Asp Ser Gly Val Ala Leu Pro	Gly Tyr Trp Met	Leu Phe Val Met Asn
610	615	620
Ser Ala Gly Val Pro Ser Val Ala Ser Thr	Ile Arg Val Thr Gln	
625	630	635

<210> 21
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 4.F12 (N413D, S550, V494A, S610) from D.
 Dendroides GaO

<400> 21		
Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp	Ala Val	
1 5 10 15		
Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys	Ala Ile Asp	
20 25 30		
Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp		
35 40 45		
Pro Lys Pro Pro His Thr Tyr Ile Asp Met Lys Thr Thr Gln Asn		
50 55 60		
Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly		
65 70 75 80		
Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp		
85 90 95		
Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys		
100 105 110		
Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala		
115 120 125		
Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn		
130 135 140		
Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg		
145 150 155 160		
Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ile		
165 170 175		
Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp		
180 185 190		
Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp		
195 200 205		
Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His		
210 215 220		
Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val		
225 230 235 240		
Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser		
245 250 255		
Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr		
260 265 270		
Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly		
275 280 285		
Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro		

290	295	300													
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310						315				320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
					325				330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
					340			345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
					355			360				365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
					370			375				380			
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
					385			390		395				400	
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asp	Ala	His	Ile
					405			410				415			
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
					420			425				430			
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
					435			440				445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
					450			455				460			
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
					465			470		475				480	
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
					485			490				495			
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
					500			505				510			
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
					515			520				525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
					530			535				540			
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
					545			550		555				560	
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
					565			570				575			
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
					580			585				590			
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
					595			600				605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
					610			615				620			
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
					625			630				635			

<210> 22

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Vector sequence

<400> 22

aagctatgtt 10
<210> 23
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 23
ttcgatcgaa 10
<210> 24
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 24
gaatttaattc 10
<210> 25
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 25
cttaatttaag 10
<210> 26
<211> 9
<212> PRT
<213> Dactylium dendroides

<400> 26
Met Ala Ser Ala Pro Ile Gly Ser Ala
1 5

<210> 27
<211> 27
<212> DNA
<213> Dactylium dendroides

<400> 27
atggcctcag cacctatcg aagcgcc 27
<210> 28

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<222> (1)...(27)
<223> "n" at positions 6, 9, 12, 15, and 21 is either a, t, g, or c.
"n" at position 18 is either a, t, or c.

<223> Randomly altered D. Dendoides wild-type sequence

<400> 28
atggcncnctcng cncccnatngg nagcgcc 27

<210> 29
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 29
aggaaaaagct tatg 14

<210> 30
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 30
aggaaaaaaagc ttatg 15

<210> 31
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 31
aggaaaaacaag cttatg 16

<210> 32
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 32
aggaacaaag cttatg 16

<210> 33
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 33
agggaaaagct tatg 14

<210> 34
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 34
aggaaaaaggc ttatg 15

<210> 35
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 35
aggaaaacaag cttatg 16

<210> 36
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 36
aggaacaaag cttatg 16

<210> 37
<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 9.16.8D2 (A1609G) of D. Dendroides GaO

<400> 37

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaaacgg	ggatccaaag	ccccctcaca	catacacgt	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgcatacg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcatatggca	caaactgggg	cagccctgtt	300
gcgtcaggt	gttggttcgc	cgactctact	acaaaataact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgc	cgctatcact	gaagcgaatg	gccagccttgc	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtcc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtgg	600
atcactttga	cgtcttcctg	ggatccatcc	actggatattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccttgtt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcg	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtggtg	atgtgaagtc	agccggaaaa	cggcagtcta	accgtgggt	agccctgtat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gcccgttaaag	gaaagatcct	gacccttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaaccggaa	catctccaa	cactgtctt	getagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacaccc	ctgttgttct	tccagacgga	agcacgttta	ttacaggagg	ccaaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccgta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	tctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggt	ggtgggtggc	tttggcgttgc	ttgttaccacg	1560
aatcatttcg	acgcgc当地	ctttacgcca	aactatctt	acaatagcga	cgccaaatctc	1620
gacacacgtc	ccaagattac	cagaaccctt	acacagagcg	tcaaggtcgg	tgccagaatt	1680
acaatctcga	cggattttc	gattagcaag	gggtcggttgc	ttcgctatgg	tacagcgaca	1740
cacacggta	atactgacca	gcccgcatt	ccccgtactc	tgacaaaacaa	tggaggaaat	1800
agctattctt	tccaaaggcc	tagcgactt	gggttgctt	tgccctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttccctag	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 38

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 9.16.6C11 (T1481C, T1543A) of D. Dendroides
GaO

<400> 38

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaaacgg	ggatccaaag	ccccctcaca	catacacgt	tgacatgaag	180

acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggt	gttggttcgc	cgactctact	acaaaatact	ccaaacttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatca	gaagcgaatg	gccagcctt	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtcc	ttatgtggc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctg	gatccatcc	actggatttg	tttccgaccg	cactgtgaca	660
gtcacccaagc	atgatatgtt	ctgccttgg	atctccatgg	atgtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccggac	ctgacatgca	agtggctcg	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgtt	ttaccattgg	aggctctgg	agcggggcg	tatttggaaa	gaatggcgaa	900
gtctatacgcc	catcttcaaa	gacatggacg	tccttaccca	atgccaagg	caacccaatg	960
ttgacggctg	acaaggcaagg	attgtaccgt	tcagacaacc	acgcgtgg	cttggatgg	1020
aagaagggtt	cgggttcca	agcgggac	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggt	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgg	agccctgtat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacccttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctccaa	cactgtctt	gtagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacac	ctgttgg	tccagacgga	agcacgtt	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccgta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaaggcagaa	ccccaaactcc	atgttcgcg	cctaccatag	cattccctt	1500
ttgttacctg	atggcagggt	attnaacgg	ggttgtgg	ttagtggcga	ttgttaccacg	1560
aatcatttcg	acgcgcaa	cttacgcca	aactatctt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctt	acacagagcg	tcaaggtcg	tggcagaatt	1680
acaatctcg	cggattctc	gattagcaag	gcgtcggt	ttcgctatgg	tacagcgaca	1740
cacacggta	atactgacca	gcccgcatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcactt	ggttgtg	tgcctggct	ctggatgtt	1860
ttcgtgatga	actcgccgg	tgttccatgt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 39

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 9.16.16D12 (T408C, T1481C) of D. Dendroides
GaO

<400> 39

gcctcagcac	ctatcgaa	cgccatttct	cgcaacaact	ggccgtcac	ttgcgacagt	60
gcacagtccg	gaaatgaatg	caacaaggcc	attgtatggca	acaaggatac	cttttggcac	120
acattctatg	gcgcacacgg	ggatccaaag	ccccctcaca	catacacat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggt	gttggttcgc	cgactctact	acaaaatact	ccaaacttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatca	gaagcgaatg	gccagccct	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtcc	ttatgtggc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctg	gatccatcc	actggatttg	tttccgaccg	cactgtgaca	660
gtcacccaagc	atgatatgtt	ctgccttgg	atctccatgg	atgtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780

atccgggac	ctgacatgca	agtggctcg	gggtatcagt	catcagctac	catgtcagac	840
ggcgtgttt	ttaccattgg	aggctctgg	agcggggcg	tatttgagaa	aatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaagg	caacccaatg	960
ttgacggctg	acaaggcaagg	attgtaccgt	tcagacaacc	acgcgtgg	cttggatgg	1020
aagaagggtt	cggtgttcca	agcgggac	agcacagcc	tgaactggta	ctataccagt	1080
ggaagtgg	atgtgaagtc	agccggaaaa	cggcgtct	accgtgg	agccctgtat	1140
gccatgtcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacccttggc	1200
ggctccccag	attatcaaga	ctctgaccc	acaaccaacg	cccacatcat	caccctcggt	1260
gaaccggaa	catctccaa	cactgtctt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacac	ctgttgttct	tccagacgga	agcacgtt	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccgta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacacttct	acaaggcagaa	ccccaaactcc	attgttcg	cctaccatag	cattccctt	1500
ttgttacctg	atggcagggt	atttaacgg	ggtgggtgg	tttggcga	ttgttaccacg	1560
aatcatttcg	acgcgcaa	cttacgcca	aactatctt	acaatagcaa	cggcaatctc	1620
gacacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaaggtcgg	tggcagaatt	1680
acaatctcg	cggattctt	gattagcaag	gogtcgttga	ttcgctatgg	tacagcgaca	1740
cacacggta	atactgacca	gcccgcatt	cccctgactc	tgacaaaacaa	tggaggaaat	1800
agctattctt	tccaaagtcc	tagcgactct	ggttgc	tgcctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcc	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 40

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 11.03.6D3 (T28C, T408C, T1481C) of D. Dendroides GaO

<400> 40

gcctcagcac	ctatcggaag	cggcattcct	cgcaacaact	gggcccgtcac	ttgcgacagt	60
gcacagtccg	gaaatgaatg	caacaaggcc	attgtggca	acaaggatac	cttttggcac	120
acattctatg	gcccacacgg	ggatccaaag	ccccctcaca	catacacat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgagg	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gctcaggt	gttgggtcgc	cgactctact	acaaaataact	ccaacttga	aactcgccct	360
gctcgctatg	ttcgtcttgc	cgctatca	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtcc	ttatgtggc	ttcatatcgc	aatgtatgc	ttggaggatc	ccctgggtgt	600
atcacttga	cgtcttctg	gatccatcc	actggattt	tttccgacc	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccttgtt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atccgggac	ctgacatgca	agtggctcg	gggtatcagt	catcagctac	catgtcagac	840
ggcgtgttt	ttaccattgg	aggctctgg	agcggggcg	tatttgagaa	aatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaagg	caacccaatg	960
ttgacggctg	acaaggcaagg	attgtaccgt	tcagacaacc	acgcgtgg	cttggatgg	1020
aagaagggtt	cggtgttcca	agcgggac	agcacagcc	tgaactggta	ctataccagt	1080
ggaagtgg	atgtgaagtc	agccggaaaa	cggcgtct	accgtgg	agccctgtat	1140
gccatgtcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacccttggc	1200
ggctccccag	attatcaaga	ctctgaccc	acaaccaacg	cccacatcat	caccctcggt	1260
gaaccggaa	catctccaa	cactgtctt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacac	ctgttgttct	tccagacgga	agcacgtt	ttacaggagg	ccaacgacgt	1380

ggaattccgt	tcgaggattc	aaccccgt	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaaggcagaa	ccccaaactcc	attgttcgcg	cctaccata	cattccctt	1500
ttgttacctg	atggcagggt	attnaacgg	ggtgggtggc	tttggcgttgc	ttgttaccacg	1560
aatcatttcg	acgcgc当地	cttacgcca	aactatctt	acaatagcaa	cggaatctc	1620
gacacacgtc	ccaagattac	cagaacctt	acacagagcg	tcaaggtcgg	tggcagaatt	1680
acaatctcg	cgattttc	gattagcaag	gctcggttgc	ttcgctatgg	tacagcgaca	1740
cacacggtt	atactgacca	gcccgcatt	ccctgactc	tgacaaacaa	tggagggaaat	1800
agctattctt	tccaagttcc	tagcgactt	ggtgttgctt	tgctggcta	ctggatgttg	1860
ttcgtatga	actcgccgg	tgttccctgt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 41

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 11.03.10C3 (A9C, T408C, G584A, T1481C) of
D. Dendroides GaO

<400> 41

gcctcagccc	ctatcggaa	cgccatttct	cgcaacaact	ggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgtatggca	acaaggatac	cttttggcac	120
acattctatg	gcccacacgg	gatccaaag	ccccctcaca	catacacat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgcataat	ctgcctcgc	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgagg	ttatctaagc	tcaagatggca	caaactgggg	cagccctgtt	300
gcgtcaggt	gttggttcgc	cgactctact	acaaaataact	ccaaacttga	aactcgccct	360
gctcgctatg	ttcgttctgt	cgctatca	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttt	tacacagccc	cccagcctgg	tcttggacgc	480
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atcactttga	cgttccctg	gatccatcc	actggattt	tttccgaccg	cactgtgaca	660
gtcaccacgc	atgatatgtt	ctgcccctgt	atctccatgg	atgtaacgg	tcagatcgta	720
gtcacaggt	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccccggac	ctgacatgca	agtggctcgt	ggttatca	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaagg	caacccaatg	960
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aagaagggtt	cggtgttcca	agcgggaccc	agcacagcc	tgaactggta	ctataccagt	1080
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gccatgtgcg	gaaacgtgt	catgtacgac	gccgttaaag	gaaagatcct	gaccttggc	1200
ggctccccag	attatcaaga	ctctgaccc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctccaa	cactgtctt	gctagcaatg	ggttgtactt	tgcccgaaacg	1320
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aatcatttcg	acgcgc当地	cttacgcca	aactatctt	acaatagcaa	cggaatctc	1620
gacacacgtc	ccaagattac	cagaacctt	acacagagcg	tcaaggtcgg	tggcagaatt	1680
acaatctcg	cgattttc	gattagcaag	gctcggttgc	ttcgctatgg	tacagcgaca	1740
cacacggtt	atactgacca	gcccgcatt	ccctgactc	tgacaaacaa	tggagggaaat	1800
agctattctt	tccaagttcc	tagcgactt	ggtgttgctt	tgctggcta	ctggatgttg	1860
ttcgtatga	actcgccgg	tgttccctgt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 42
<211> 1917
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant 11.03.10D6 (T408C, T654C, A936G, T1481C, A1603G) of D. Dendroides GaO

<400> 42

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gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcccacaacgg	gatccaaag	ccccctcaca	catacacatg	tgacatgaag	180
acaactcaga	acgtcaacgg	ttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcaact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtcc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctg	gatccatcc	actggatttg	tttccgaccg	caccgtgaca	660
gtcacaaggc	atgatatgtt	ctgccctgg	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcg	ggttatca	catcagctac	catgtcagac	840
ggtcgtgtt	ttaccattgg	aggctcctgg	agcggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctgcca	atgccaaggt	caacccaatg	960
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gccatgtgct	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gaccttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaaccggaa	catctccaa	cactgtctt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
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gacactttct	acaaggcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
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cacacggta	atactgacca	gcccgcatt	cccctgactc	tgacaaaacaa	tggagggaaat	1800
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ttcgtgatga	actcgccgg	tgttccctagt	gtggcttcga	cgattcgctgt	tactcag	1917

<210> 43
<211> 1917
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant 11.03.13E12 (A208G, T408C, T1481C) of D. Dendroides GaO

<400> 43

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gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaaacgg	ggatccaaag	ccccctcaca	catacacgt	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctgt	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggt	gttggttcgc	cgactctact	acaaaataact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtcc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggttgt	600
atcactttga	cgtcttcctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccttgtt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcg	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtggtgt	agcccctgat	1140
gccatgtgog	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gaccttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaaccggaa	catctccaa	cactgttctt	getagcaatg	ggttgtactt	tgcccgaacg	1320
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ggaattccgt	tcgaggattc	aaccccggt	tttacacctg	agatctacgt	ccctgaacaa	1440
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acaatctcga	cggattttc	gattagcaag	ggtcggttga	ttcgctatgg	tacagcgaca	1740
cacacggta	atactgacca	gcccgcatt	cccctgactc	tgacaaaacaa	tggagggaaat	1800
agctattctt	tccaaaggcc	tagcgactct	ggtgttgctt	tgcctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttccttagt	gtggcttcga	cgattcgcgt	tactcg	1917

<210> 44

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 1.06.20E7 (T28C, A208G, T408C, G584A, T1481C, A1603G) of D. Dendroides GaO

<400> 44

gcctcagcac	ctatcggaaag	cgccatttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaaacgg	ggatccaaag	ccccctcaca	catacacgt	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctgt	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggt	gttggttcgc	cgactctact	acaaaataact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtcc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttgaaggatc	ccctgggttgt	600

atcactttga	cgtcttcctg	ggatccatcc	actggatttg	tttccgaccg	cactgtgaca	660
gtcacccaagc	atgatatgtt	ctgcccgtt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgac	ctgacatgca	agtggctcgt	ggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatacgcc	catcttcaaa	gacatggacg	tccctaccca	atgccaagg	caacccaatg	960
ttgacggctg	acaaggcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggt	atgtgaagtc	agccggaaaa	cggcagtcta	accgtgggt	agcccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacccttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaaccggaa	catctccaa	cactgtctt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
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ggaattccgt	tcgaggattc	aaccccgta	tttacacctg	agatctacgt	ccctgaacaa	1440
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ttgttacctg	atggcagggt	atttaacgg	ggtgggtgtc	tttgtggcga	ttgttaccacg	1560
aatcatttcg	acgcgcaaatt	ctttacgcc	aactatctt	acgatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaaggtcg	tggcagaatt	1680
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cacacggta	atactgacca	gcccgcatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaaaggttcc	tagcgactc	ggtgttgctt	tgcctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttccctag	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 45

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 1.D4 (A1237G) of D. Dendroides GaO

<400> 45

gcctcagcac	ctatcgaaag	cggcatttct	cgcacaact	ggccgtcac	ttgcgacagt	60
gcacagtccg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	ctttggcac	120
acattctatg	gcccacacgg	ggatccaaag	ccccctcaca	catacacat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgcctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggt	gttggttcgc	cgactctact	acaaaatact	ccaaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgc	cgctatca	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtcc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggttgt	600
atcactttga	cgtcttcctg	ggatccatcc	actggatttg	tttccgaccg	cactgtgaca	660
gtcacccaagc	atgatatgtt	ctgcccgtt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgac	ctgacatgca	agtggctcgt	ggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatacgcc	catcttcaaa	gacatggacg	tccctaccca	atgccaagg	caacccaatg	960
ttgacggctg	acaaggcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggt	atgtgaagtc	agccggaaaa	cggcagtcta	accgtgggt	agcccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacccttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccgacg	cccacatcat	caccctcggt	1260

gaaccggaa	catctccaa	cactgtctt	gctagcaatg	ggttgtactt	tgcggaaacg	1320
tttcacac	ctgttgc	tccagacgg	agcacgtt	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggt	tttacac	agatctacgt	ccctgaacaa	1440
gacacttct	acaagcagaa	ccccaaactcc	attgttgc	tctaccatag	catttccctt	1500
ttgttac	atggcagggt	atttaac	ggtgtggc	tttgtggcga	ttgtaccacg	1560
aatcattcg	acgcgcaa	cttacgca	aactatctt	acaatagcaa	cggcaatctc	1620
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agctattctt	tccaaagtcc	tagcgactc	ggtgttg	tgctggcta	ctggatgtt	1860
ttcgtgatga	actcgccgg	tgttcc	gtggctc	cgattcgcgt	tactcag	1917

<210> 46

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 2.G4 (A1237G, T1650A) of D. Dendroides GaO

<400> 46

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gcacagtcgg	gaaatgaatg	caacaaggcc	attgtatggca	acaaggatac	cttttggcac	120
acattctatg	gcccacacgg	ggatccaaag	ccccctcaca	catacacgt	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgc	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgagg	ttatcta	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggta	gttgggtcgc	cgactctact	acaaaataact	ccaacttga	aactcgccct	360
gctcgctatg	ttcgtctt	cgctatca	gaagcgaatg	gccagcctt	gactagcatt	420
gcagagatca	acgtcttcca	agctagt	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cotgcggctg	cagcaattga	accgacatcg	540
ggacgagtcc	ttatgtggc	ttcatat	aatgtatgc	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttcc	gatccatcc	actgg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgc	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagg	gcaacgatgc	caagaagacc	agttt	attcatctag	cgatagctgg	780
atccgggac	ctgacatgca	agtggctcg	gg	catcagctac	catgtcagac	840
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gtctatagcc	catcttcaa	gacatggac	tc	atgccaagg	caacccaaatg	960
ttgacggctg	acaagcaagg	attgtac	tc	acgcgtgg	cttggatgg	1020
aagaagggtt	cgtgttcca	agcgggac	agc	tgaactgg	ctataccagt	1080
ggaagtgg	atgtgaagtc	agccggaaa	cgc	accgtgg	agcccctgat	1140
gccatgtcg	gaaacgctgt	catgtac	gcgtt	gaaagatcc	gac	1200
ggctccccag	attatcaaga	ctctgac	acaacc	cc	cac	1260
gaacccggaa	catctccaa	cactgtctt	gct	accatcat	cctcg	1320
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ggaattccgt	tcgaggattc	aaccccggt	tttacac	at	cc	1440
gacacttct	acaagcagaa	ccccaaactcc	attgttgc	tct	at	1500
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aatcattcg	acgcgcaa	cttacgca	aactat	aca	cg	1620
gacacacgtc	ccaagattac	cagaac	acacag	tca	tgg	1680
acaatctcg	cggattt	gattagcaag	gcgtcg	tgc	cagaatt	1740
cacacggta	atactgacca	gcccgcatt	ccc	tgacaaacaa	tggagaaat	1800
agctattctt	tccaaagtcc	tagcgactc	ggtgttg	tgctgg	ctggatgtt	1860
ttcgtgatga	actcgccgg	tgttcc	gtggctc	cgattcgcgt	tactcag	1917

<210> 47
<211> 1917
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant 3.H7 (A1237G, T1650A, T1481C) of D.
Dendroides GaO

<400> 47

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gcacagtccg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaaacgg	gatccaaag	ccccctcaca	catacacat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgcatacg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
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